RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/661,809A

Source: IFW016

Date Processed by STIC: 6/26/06

ENTERED

RAW SEQUENCE LISTING   DATE: 06/26/2006
PATENT APPLICATION: US/10/661,809A   TIME: 11:36:21

Input Set : A:\PTO.DA.txt
Output Set: N:\CRF4\06262006\J661809A.raw


```
   3 <110> APPLICANT: HOOK, Magnus
   5 <120> TITLE OF INVENTION: BIOINFORMATIC METHOD FOR IDENTIFYING SURFACE-ANCHORED
PROTEINS FROM GRAM-
   6        POSITIVE BACTERIA
   8 <130> FILE REFERENCE: P07741US01/BAS
  10 <140> CURRENT APPLICATION NUMBER: 10/661809A
  11 <141> CURRENT FILING DATE: 2003-09-15
  13 <150> PRIOR APPLICATION NUMBER: 60/410303
  14 <151> PRIOR FILING DATE: 2002-09-13
  16 <160> NUMBER OF SEQ ID NOS: 57
  18 <170> SOFTWARE: PatentIn version 3.1
  20 <210> SEQ ID NO: 1
  21 <211> LENGTH: 5
  22 <212> TYPE: PRT
  23 <213> ORGANISM: Staphylococcus epidermidis
  25 <220> FEATURE:
  26 <221> NAME/KEY: MISC_FEATURE
  27 <222> LOCATION: (3)..(3)
  28 <223> OTHER INFORMATION: X = any amino acid
  31 <400> SEQUENCE: 1
W--> 33 Leu Pro Xaa Thr Gly
  34 1               5
  37 <210> SEQ ID NO: 2
  38 <211> LENGTH: 777
  39 <212> TYPE: PRT
  40 <213> ORGANISM: Staphylococcus epidermidis
  42 <400> SEQUENCE: 2
  44 Gln Glu Gln Thr Ala Lys Glu Asp Val Ala Asp Ser Ala Thr Ser Val
  45 1               5                   10                  15
  48 Gly Ala Ile Val Ser Ile Glu Lys Ala Glu Lys Asn Phe Val Ile Thr
  49             20                  25                  30
  52 Tyr Ala Ser Gly Lys Lys Ala Gln Ile Ser Ile Leu Asn Asp His Leu
  53         35                  40                  45
  56 Phe Arg Tyr His Leu Asp Pro Thr Gly Lys Phe Glu Glu Tyr Pro Thr
  57     50                  55                  60
  60 Pro Asn Asp Pro Lys His Val Ala Lys Ile Thr Ala Lys Thr Met Ala
  61 65                  70                  75                  80
  64 Asp Tyr Gly Thr Gln Ala Phe Glu Gln Thr Asn Val Thr Asp Ser Gly
  65             85                  90                  95
  68 Asn Gln Phe Ile Leu Glu Asn Asn Gly Leu Lys Ile Met Phe Glu Lys
  69             100                 105                 110
  72 Glu Ser Ala Leu Met Lys Val Leu Asp Lys Lys Lys Asn Gln Val Ile
  73         115                 120                 125
  76 Leu Glu Glu Thr Ala Pro Leu Ser Phe Lys Asn Asp Lys Ala Thr Gln
```

```
77      130                   135                   140
80  Thr Leu Lys Gln Ser Ser Gln Glu Asn Tyr Phe Gly Gly Gly Thr Gln
81  145               150                   155                   160
84  Asn Gly Arg Phe Thr His Lys Gly Thr Ala Ile Gln Ile Val Asn Thr
85               165                   170                   175
88  Asn Asn Trp Val Asp Gly Gly Val Ala Ser Pro Asn Pro Phe Tyr Trp
89.     .        180                   185             ....190
92  Ser Thr Ala Gly Tyr Gly Val Val Arg Asn Thr Trp Lys Pro Gly Asn
93            195                   200                   205
96  Tyr Asp Phe Gly Ser His Asp Pro Gln Lys Thr Thr Thr Thr His Glu
97       210                   215                   220
100 Gly Thr Asp Phe Asp Ala Phe Tyr Phe Phe Asn Asp Ser Ser Ala Gly
101 225                   230                   235                   240
104 Ile Leu Lys Asp Tyr Tyr Glu Leu Thr Gly Lys Pro Ala Leu Met Pro
105               245                   250                   255
108 Glu Tyr Gly Phe Tyr Glu Ala His Leu Asn Ala Tyr Asn Arg Asp Tyr
109            260                   265                   270
112 Trp Val Lys Val Ala Glu Gly Thr Ala Gly Ala Val Lys Phe Glu Asp
113          275                   280                   285
116 Gly Asn Phe Tyr Lys Glu Tyr Gln Pro Gly Asp Leu Gly Asn Leu Asn
117       290                   295                   300
120 Gly Thr Leu Glu Ser Leu Asn Gly Glu Lys Glu Asn Tyr Gln Phe Ser
121 305                   310                   315                   320
124 Ala Arg Ala Val Ile Asp Arg Tyr Lys Lys Asn Asp Met Pro Leu Gly
125               325                   330                   335
128 Trp Phe Leu Pro Asn Asp Gly Tyr Gly Ala Gly Tyr Gly Gln Thr Asp
129            340                   345                   350
132 Ser Leu Asp Gly Asp Val Gln Asn Leu Lys Glu Phe Thr Glu Tyr Ala
133          355                   360                   365
136 Gln Ala Asn Gly Val Glu Val Gly Leu Trp Thr Gln Ser Asn Leu His
137       370                   375                   380
140 Pro Ala Asp Pro Lys Asn Pro Lys Lys Gly Glu Arg Asp Ile Ala Lys
141 385                   390                   395                   400
144 Glu Val Ser Val Ala Gly Val Lys Ala Leu Lys Thr Asp Val Ala Trp
145               405                   410                   415
148 Val Gly Tyr Gly Tyr Ser Phe Gly Leu Asn Gly Val Glu Asp Ala Ala
149            420                   425                   430
152 Asn Val Phe Val Lys Glu Thr Asp Gly Ala Val Arg Pro Met Ile Val
153          435                   440                   445
156 Ser Leu Asp Gly Trp Ala Gly Thr Gln Arg His Ala Gly Ile Trp Thr
157     450                   455                   460
160 Gly Asp Gln Thr Gly Gly Gln Trp Glu Tyr Ile Arg Phe His Ile Pro
161 465               470                   475                   480
164 Thr Tyr Ile Gly Thr Ser Leu Ser Gly Gln Pro Asn Val Gly Ser Asp
165            485                   490                   495
168 Met Asp Gly Ile Phe Gly Gly Lys Asn Lys Glu Ile Asn Ile Arg Asp
169            500                   505                   510
172 Phe Gln Trp Lys Thr Phe Thr Pro Val Gln Leu Asn Met Asp Gly Trp
173          515                   520                   525
```

```
176 Gly Ser Asn Pro Lys Thr Pro Phe Ala Phe Asp Gln Glu Ala Thr Asp
177     530                 535                 540
180 Leu Asn Arg Ala Tyr Leu Lys Leu Lys Ser Met Met Met Pro Tyr Asn
181 545                 550                 555                 560
184 Tyr Ser Ile Ala Lys Glu Ser Val Asp Gly Leu Pro Met Val Arg Ala
185                 565                 570                 575
188 Met Ala Leu Glu Phe Pro Asn Glu Gly Thr Ala Tyr Thr Lys Asp Ser
189             580                 585                 590
192 Gln Tyr Gln Tyr Met Trp Gly Pro Asn Leu Leu Val Ala Pro Ile Tyr
193             595                 600                 605
196 Asn Gly Asn Gln Asp Glu Ala Gly Asn Ser Ile Arg Asp Gly Ile Tyr
197     610                 615                 620
200 Leu Pro Asp Glu Lys Gln Val Trp Val Asp Leu Phe Thr Gly Glu Lys
201 625                 630                 635                 640
204 Tyr Gln Gly Gly Arg Val Leu Asn Gly Val Lys Thr Pro Leu Trp Lys
205                 645                 650                 655
208 Val Pro Val Phe Val Lys Asp Gly Ser Ile Ile Pro Met Thr Asn Pro
209             660                 665                 670
212 Asn Asn Asn Pro Lys Glu Ile Gln Arg Asp Gln Arg Ser Phe Leu Ile
213         675                 680                 685
216 Tyr Pro Asn Gly Thr Thr Ser Phe Asn Met Tyr Glu Asp Asp Gly Ile
217     690                 695                 700
220 Ser Thr Ser Tyr Glu Ala Gly Gln Ser Ala Thr Thr Lys Ile Asn Ser
221 705                 710                 715                 720
224 Gln Gly Pro Lys Ser Asn Glu Lys Gly Asp Leu Thr Val Thr Ile Glu
225             725                 730                 735
228 Pro Thr Lys Gly Ser Tyr Lys Asp Phe Val Asp Glu Arg Ser Thr Thr
229             740                 745                 750
232 Leu Asp Leu Leu Ala Ser Glu Ala Pro Glu Ser Val Thr Ala Met Val
233         755                 760                 765
236 Gly Gly Thr Glu Val Thr Leu Lys Gln
237     770                 775
240 <210> SEQ ID NO: 3
241 <211> LENGTH: 1010
242 <212> TYPE: PRT
243 <213> ORGANISM: Staphylococcus epidermidis
245 <400> SEQUENCE: 3
247 Ala Ala Asn Lys Glu Glu Phe Leu Ala Gly Thr Asn Leu Tyr Tyr Phe
248 1               5                   10                  15
251 Asp Lys Glu Phe Gln Val Asn Gln Tyr Leu Ser Glu Ala Ser Gly Glu
252             20                  25                  30
255 Lys Leu Asn Gln Ser Ala Leu Ser Val Lys Leu Ala Lys Gln Ser Val
256         35                  40                  45
259 Thr Ala Lys Asp Val Gln Ile Thr Val Lys Gly Phe Ile Asn Lys Gly
260     50                  55                  60
263 Thr Val Asp Gly Gly Asn Thr Thr Val Asp Asp Gln Leu Thr Ile Pro
264 65                  70                  75                  80
267 Ala Asn Val Ala Ile Asn Glu Glu Lys Thr Thr Pro Ser Ser Leu Thr
268             85                  90                  95
```

RAW SEQUENCE LISTING   DATE: 06/26/2006
PATENT APPLICATION: US/10/661,809A   TIME: 11:36:21

Input Set : **A:\PTO.DA.txt**
Output Set: **N:\CRF4\06262006\J661809A.raw**

```
271 Leu Gln Trp Asp Gln Val Thr Glu Ala Thr Ser Tyr Glu Val Glu Arg
272             100                 105                 110
275 Asp Gly Thr Val Phe Gly Asn Ile Gln Thr Asn Thr Ala Thr Phe Asp
276             115                 120                 125
279 Gly Phe Ser Phe Leu Ser Glu His Thr Phe Arg Val Arg Ala Val Gly
280         130                 135                 140
283 Lys Asn Gly Val Ser Glu Trp Ser Glu Pro Ile Lys Gly Lys Thr Gln
284 145                 150                 155                 160
287 Asp Asp Pro Tyr Lys Glu Thr Ile Asn Gln Val Lys Ala Thr Ser Asn
288             165                 170                 175
291 Leu Pro Glu Gln Pro Gly Ala Glu Leu Lys Lys Leu Thr Asp Lys Asp
292             180                 185                 190
295 Leu Ser Thr Gly Trp His Thr Asn Trp Ser Thr Gly Ile Ala Asn Pro
296             195                 200                 205
299 Ser Asp Gly Asn Phe Leu Ser Leu Lys Phe Asp Leu Gly Ala Glu Tyr
300         210                 215                 220
303 Gln Met Asp Lys Ile Glu Tyr Leu Pro Arg Asp Asn Ala Gly Asn Gly
304 225                 230                 235                 240
307 Asn Ile Leu Gln Leu Gln Tyr Arg Thr Ser Lys Asp Gly Ala Asn Trp
308             245                 250                 255
311 Thr Glu Phe Ser Glu Pro Ile Asn Trp Lys Gln Asp Ala Leu Thr Lys
312             260                 265                 270
315 Thr Ile Glu Thr Lys Asp Gln Ala Tyr Arg Phe Val Glu Met Lys Val
316         275                 280                 285
319 Leu Lys Ser Val Gly Asn Phe Gly Ser Gly Arg Glu Met Leu Phe Tyr
320     290                 295                 300
323 Lys Gln Pro Gly Thr Glu Gly Ile Leu His Gly Asp Ile Thr Asn Asp
324 305                 310                 315                 320
327 Gly Thr Ile Asp Glu Asn Asp Ala Met Ser Tyr Arg Asn Tyr Thr Gly
328             325                 330                 335
331 Leu Glu Ser Val Asp Ser Asp Phe Asn Gly Tyr Val Glu Lys Gly Asp
332             340                 345                 350
335 Leu Asn Lys Asn Gly Val Ile Asp Ala Tyr Asp Ile Ser Tyr Val Leu
336         355                 360                 365
339 Arg Gln Leu Asp Gly Gly Ile Glu Ile Pro Asp Val Glu Glu Ile Ala
340     370                 375                 380
343 Gly Gly Leu Ser Leu Ala Val Val Asn Glu Asn Gly Lys Asp Thr Tyr
344 385                 390                 395                 400
347 Leu Pro Gly Asp Thr Leu Thr Phe Ile Leu Lys Gly Gln Asp Leu Lys
348             405                 410                 415
351 Asn Ile Asn Ala Leu Ser Thr Lys Met Ser Phe Asp Ser Ser Lys Phe
352         420                 425                 430
355 Glu Leu Val Gly Gln Pro Ala Thr Thr Asn Asn Thr Gln Gln Met Glu
356         435                 440                 445
359 Asn Tyr Ser Lys Tyr Arg Lys His Ser Asn Asp Val Glu Asn Leu Tyr
360     450                 455                 460
363 Leu Val Leu Ser Asn Gln Gly Asn Lys Gln Leu Leu Asn Gly Ser Met
364 465                 470                 475                 480
367 Asp Leu Val Thr Phe Lys Val Lys Val Lys Glu Thr Thr Arg Val Lys
```

```
368                  485                  490                  495
371 Arg Ala Thr Thr Val Glu Gln Pro Leu Gln Phe Asp Met Ser Gln Gly
372              500                  505                  510
375 Leu Leu Val Gly Gln Gly Phe Gln Gln Ala Thr Leu Ser Asp Phe Ser
376          515                  520                  525
379 Val Thr Val Lys Pro Thr Glu Leu Val Asp Lys Glu Leu Leu Gln Ala
380          530                  535                  540
383 Leu Ile Thr Leu Asn Gln Ala Arg Val Glu Lys Glu Tyr Thr Pro Glu
384 545                  550                  555                  560
387 Thr Trp Ala Ile Phe Lys Pro Ile Leu Asp Glu Ala Val Ala Val Leu
388          565                  570                  575
391 Ala Asn Glu Gln Ala Thr Gln Thr Asp Val Ser Ala Ala Ala Glu Asn
392          580                  585                  590
395 Leu Glu Lys Ala Ala Ser Gln Leu Glu Lys Met Pro Asp Val Ala Asn
396          595                  600                  605
399 Lys Ala Asp Leu Glu Lys Ala Ile Gln Glu Gly Leu Ala Lys Lys Pro
400      610                  615                  620
403 Ser Asp Gly Gln Glu Phe Thr Glu Glu Thr Lys Lys Val Leu Glu Glu
404 625                  630                  635                  640
407 Ser Leu Ala Ala Ala Gln Lys Val Phe Ala Gln Glu Lys Val Thr Gln
408          645                  650                  655
411 Glu Glu Ile Asp Gln Ala Thr Lys Thr Leu Arg Glu Ala Ile Ala Gln
412          660                  665                  670
415 Leu Lys Glu Gln Pro Val Ala Val Asp Lys Glu Thr Leu Lys Glu Gln
416          675                  680                  685
419 Ile Ala Gln Ala Arg Gly Arg Lys Pro Glu Glu Gly Tyr Gln Phe Thr
420      690                  695                  700
423 Lys Glu Thr Glu Lys Gln Leu Gln Glu Ala Ile Gln Ala Ala Glu Ala
424 705                  710                  715                  720
427 Ile Val Ala Lys Glu Thr Ala Thr Lys Glu Glu Val Ser Glu Ala Leu
428          725                  730                  735
431 Asn Ala Leu Glu Thr Ala Met Ala Gln Leu Lys Glu Val Pro Leu Val
432          740                  745                  750
435 Asn Lys Asp Gln Leu Gln Glu Val Val Lys Arg Ala Gln Gln Val Thr
436          755                  760                  765
439 Pro Ser Glu Gly His Gln Phe Thr Ala Ser Ser Leu Gln Glu Leu Gln
440      770                  775                  780
443 Lys Ala Leu Leu Ala Ala Lys Asn Thr Leu Lys Asn Pro Ala Ala Asn
444 785                  790                  795                  800
447 Gln Lys Met Ile Asp Glu Ala Val Ala Glu Leu Thr Ser Ala Ile Asp
448          805                  810                  815
451 Gly Leu Gln Glu Glu Val Leu Val Thr Asp Lys Lys Ala Leu Glu Ala
452          820                  825                  830
455 Met Ile Ala Lys Ala Lys Ala Ile Lys Pro Ser Ala Gly Lys Glu Phe
456          835                  840                  845
459 Thr Ser Glu Ser Lys Ala Arg Leu Thr Glu Ala Ile Asp Gln Ala Glu
460      850                  855                  860
463 Gly Ile Leu Ala Asp Lys Asn Ala Arg Gln Glu Gln Ile Asp Ile Ala
464 865                  870                  875                  880
```

RAW SEQUENCE LISTING ERROR SUMMARY　　DATE: 06/26/2006
PATENT APPLICATION:　**US/10/661,809A**　　TIME: 11:36:22

Input Set　:　**A:\PTO.DA.txt**
Output Set:　**N:\CRF4\06262006\J661809A.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 3
Seq#:25; Xaa Pos. 3

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5

VERIFICATION SUMMARY　　　　　　　　　　DATE: 06/26/2006
PATENT APPLICATION:　**US/10/661,809A**　　　TIME: 11:36:22

Input Set :　**A:\PTO.DA.txt**
Output Set: **N:\CRF4\06262006\J661809A.raw**

L:33 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:7682 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0